

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/581,158  
Source: FFBP  
Date Processed by STIC: 6/9/06

# ***ENTERED***



IFWP

**RAW SEQUENCE LISTING**

DATE: 06/09/2006

PATENT APPLICATION: US/10/581,158

TIME: 10:35:46

Input Set : A:\sequence listing.DOC

Output Set: N:\CRF4\06092006\J581158.raw

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3 <110> APPLICANT: Yoshinori Watanabe
5 <120> TITLE OF INVENTION: Novel centromeric protein SHUGOSHIN
7 <130> FILE REFERENCE: 4439-4043
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/581,158
C--> 9 <141> CURRENT FILING DATE: 2006-05-31
9 <150> PRIOR APPLICATION NUMBER: JP2003-401943
10 <151> PRIOR FILING DATE: 2003-12-01
12 <150> PRIOR APPLICATION NUMBER: JP2004-279450
13 <151> PRIOR FILING DATE: 2004-09-27
15 <160> NUMBER OF SEQ ID NOS: 45
17 <170> SOFTWARE: PatentIn version 3.1
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20 <211> LENGTH: 960
21 <212> TYPE: DNA
22 <213> ORGANISM: yeast
24 <400> SEQUENCE: 1
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27 ttgaaaaaga aattttttaa acaaaatcgt gaaattataa aaataaatac tcagctttct      120
29 ataaaaatta gagaatctga aaacgaaatt caagatttga tacaagaaaa tttcactttg      180
31 aaaagttatt tggttaaact tgaagctcga tttcgcgaac aatctcaaac tgaggacttg      240
33 ttaaaaaact tctttcctga gatacaaacc attcacaaaa agatttcaca agtgcaaagt      300
35 ttactgaaga ttatagagaa aaagtgttca tcagatttcc tcgaagcgaa tgtaaaaagt      360
37 caattttaca cctgtgaaaa taaagattcg aaagaagatt atcagatttt gcataataaa      420
39 cgcttggagt atgtatcatt taatgatgaa cttaaaagtc tcgaaacagg gcaaccattg      480
41 tattgttttc aagattttcca aaaaaagtc catggtcctc cggctctatc tgaaaaacct      540
43 ggaaaatgta tattaaaaga taaaaccaat gcccacgtaa acaaaatacc acaagatgag      600
45 gtgaattact cattgccgca aaaaaatata accatctttt caaaggaatt aaaagaaaac      660
47 gaatttgaat ccatcaacga gggcgaaact gaagaagaaa aggctaaaac atcaaattgt      720
49 tgtgtttgta ttccttgtaa aagtgttgaa cagataactg accttaaagg acaagcaacc      780
51 ggagacagct ccccatgtga ttttgaagaa tctcaaccaa ggattaatgg acgtgaaaaa      840
53 ctaagacgat cagtcaaagt gataaactat gcaataccca gtttgcgaa taaactacga      900
55 cgagactttg acttaccatc tgatagaaaa cgcaaacgac atcccagagg caaagcataa      960
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 319
60 <212> TYPE: PRT
61 <213> ORGANISM: yeast
63 <400> SEQUENCE: 2
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66 1 5 10 15
69 Pro Met Glu Ser Leu Lys Lys Lys Phe Leu Lys Gln Asn Arg Glu Ile
70 20 25 30
73 Ile Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn
74 35 40 45

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77 Glu Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser Tyr Leu
78      50                      55                      60
81 Val Lys Leu Glu Ala Arg Phe Arg Asn Gln Ser Gln Thr Glu Asp Leu
82 65                      70                      75                      80
85 Leu Lys Asn Phe Phe Pro Glu Ile Gln Thr Ile His Lys Lys Ile Ser
86                      85                      90                      95
89 Gln Val Gln Ser Leu Leu Lys Ile Ile Glu Lys Lys Cys Ser Ser Asp
90                      100                      105                      110
93 Phe Leu Glu Ala Asn Val Lys Ser Gln Phe Thr Thr Cys Glu Asn Lys
94                      115                      120                      125
97 Asp Ser Lys Glu Asp Tyr Gln Ile Leu His Asn Lys Arg Leu Glu Tyr
98      130                      135                      140
101 Val Ser Phe Asn Asp Glu Leu Lys Ser Leu Glu Thr Gly Gln Pro Leu
102 145                      150                      155                      160
105 Tyr Cys Phe Gln Asp Phe Gln Lys Lys Val His Gly Pro Pro Ala Leu
106                      165                      170                      175
109 Ser Glu Lys Pro Gly Lys Cys Ile Leu Lys Asp Lys Thr Asn Ala His
110                      180                      185                      190
113 Val Asn Lys Ile Pro Gln Asp Glu Val Asn Tyr Ser Leu Pro Gln Lys
114      195                      200                      205
117 Asn Ile Thr Ile Phe Ser Lys Glu Leu Lys Glu Asn Glu Phe Glu Ser
118      210                      215                      220
121 Ile Asn Glu Gly Glu Thr Glu Glu Glu Lys Ala Lys Thr Ser Asn Val
122 225                      230                      235                      240
125 Cys Val Cys Ile Pro Cys Lys Ser Ala Glu Gln Ile Thr Asp Leu Lys
126                      245                      250                      255
129 Gly Gln Ala Thr Gly Asp Ser Ser Pro Cys Asp Phe Glu Glu Ser Gln
130                      260                      265                      270
133 Pro Arg Ile Asn Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile
134      275                      280                      285
137 Asn Tyr Ala Ile Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe Asp
138      290                      295                      300
141 Leu Pro Ser Asp Arg Lys Arg Lys Arg His Pro Arg Gly Lys Ala
142 305                      310                      315
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146 <211> LENGTH: 1944
147 <212> TYPE: DNA
148 <213> ORGANISM: yeast
150 <400> SEQUENCE: 3
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153 tataaggaaa ttatacgaat aagcaaggca caatcaatta gaattaaaga attgcagtta      120
155 gaaaatgaac gggttgcttc ggaaaatatc gatttgagga ctacagcgat aaacttgga      180
157 gagcaactcg aaaccgtgca aaacgaaaac gaagaaaaca aaacaaagt agctgcatta      240
159 cttaatcgat ttcatgaaga aacagataat tttttatcaa aattaagtct ttgtcagcaa      300
161 gaaatacaag acaccttcaa accagtggag gctaacttag cttacgatgt cgatacggat      360
163 tctgaagacc ttgacgagga atccgctcgtg aaagataccg aagaaataat tgagcaagct      420
165 cagcatgatg tttccttacg aaatttaagt ggaatagagg atgaaaatat aattgatgac      480
167 ggagaaactg ctataaatga acaaaaaaaaa agagaagcta atgttttttc cgacacgcaa      540
169 tcagcacctc agctaaaatc cggcaaagcc ctcccagctg attttgaaaa tccttacaat      600

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171 ctatccaatt cgaaacctgt aaataataat aatgaagata gagttgaagc ggttacttct 660
173 gaaaataaat ctatcgattc tgctcctcag gaaaaaaatc atgaatacga aatcgttagt 720
175 ccaaaatcat tatccaacaa aattaataat caagcagctg cacaagaag aaccgaagaa 780
177 gataatgcaa atggagttgc tcaagaagaa aatgagggtt cacaagaagc tcattttcat 840
179 agcagaatac aatctgatac agtaatacaa agtacacca ctaaaccgaa atgggacgtt 900
181 gacattcaaa ataaacaaat taatctggct tctgcagcta ccaatgttac cggttatgta 960
183 tcggagaccg atagtcgccc caatcgcgca aactctttgg attctgctgt ccttcttggtg 1020
185 caatcttcaa ataaaagtaa ccgaaatggg catcatattt cagatcctaa tttaaatagc 1080
187 tccatatcgt tgaagtttgc gcctgaagat actgcgcata attcattaac ttcacaagag 1140
189 aatgttgggc ctcaggttac gacgacttct ctgtcaaata tgactgttgc tgaatctcct 1200
191 cgtacagaca ctccaaggga aataaacggg ttagtagact cttctgtcac taatgggaac 1260
193 gaaaaatttt ctgtagaat aatgaatgac tctaacaaaa ttggactgaa tcctaaatct 1320
195 tttaccgacg aagagcggga aattttaaca ctttttcgaa atcctcccat gagactgtca 1380
197 agtgaacctc catcttcaaa tggattttca atagcccatc ccaataattc tccgttacgt 1440
199 ccgccatcgc tacaaggaat attgaatgct gaagatcgac cttacgaaat tgagccgtca 1500
201 cgtagctcct ttgctaccaa cgatacgggc tcctataata atttggaact tctgtcatct 1560
203 gtaacgaatt tgaaatcccc taatgagaac gatcgtgtga cgaaaactca gtcgcgaaga 1620
205 gaaacaaaag tgaaaaggcg aagaaaagct cggattcaag aaacttctga agaaagtaca 1680
207 gtagtcaatg agccaaatga aaaacctgat ggaaggagcc gaagggaacg gaaaaagggtt 1740
209 aattacgctt tgcttgatt aaggacgaaa ttaagacgga atttcgattt accttcagat 1800
211 catgtaaaaag ctaaaaaaac gagacgtgct cctaagaact ctgagaatga ttcagctacc 1860
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215 aactccgaaa cccttaattt gtaa 1944
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 647
220 <212> TYPE: PRT
221 <213> ORGANISM: yeast
223 <400> SEQUENCE: 4
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230 20 25 30
233 Ile Arg Ile Lys Glu Leu Gln Leu Glu Asn Glu Arg Leu Leu Ser Glu
234 35 40 45
237 Asn Ile Asp Leu Arg Thr Thr Ala Ile Asn Leu Glu Glu Gln Leu Glu
238 50 55 60
241 Thr Val Gln Asn Glu Asn Glu Glu Asn Lys Thr Lys Leu Ala Ala Leu
242 65 70 75 80
245 Leu Asn Arg Phe His Glu Glu Thr Asp Asn Phe Leu Ser Lys Leu Ser
246 85 90 95
249 Leu Cys Gln Gln Glu Ile Gln Asp Thr Phe Lys Pro Val Glu Ala Asn
250 100 105 110
253 Leu Ala Tyr Asp Val Asp Thr Asp Ser Glu Asp Leu Asp Glu Glu Ser
254 115 120 125
257 Val Val Lys Asp Thr Glu Glu Ile Ile Glu Gln Ala Gln His Asp Val
258 130 135 140
261 Ser Leu Arg Asn Leu Ser Gly Ile Glu Asp Glu Asn Ile Ile Asp Asp
262 145 150 155 160
265 Gly Glu Thr Ala Ile Asn Glu Gln Lys Lys Arg Glu Ala Asn Val Phe

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266				165				170				175	
269	Ser	Asp	Thr	Gln	Ser	Ala	Pro	Gln	Leu	Lys	Ser	Gly	Lys
270				180				185				190	
273	Ala	Asp	Phe	Glu	Asn	Pro	Tyr	Asn	Leu	Ser	Asn	Ser	Lys
274				195				200				205	
277	Asn	Asn	Asn	Glu	Asp	Arg	Val	Glu	Ala	Val	Thr	Ser	Glu
278				210				215				220	
281	Ile	Asp	Ser	Ala	Pro	Gln	Glu	Lys	Asn	His	Glu	Tyr	Glu
282	225					230					235		240
285	Pro	Lys	Ser	Leu	Ser	Asn	Lys	Ile	Asn	Asn	Gln	Ala	Ala
286				245				250				255	
289	Arg	Thr	Glu	Glu	Asp	Asn	Ala	Asn	Gly	Val	Ala	Gln	Glu
290				260				265				270	
293	Gly	Ser	Gln	Glu	Ala	His	Phe	His	Ser	Arg	Ile	Gln	Ser
294				275				280				285	
297	Ile	Gln	Ser	Thr	Pro	Thr	Lys	Arg	Lys	Trp	Asp	Val	Asp
298				290				295				300	
301	Lys	Gln	Ile	Asn	Leu	Ala	Ser	Ala	Ala	Thr	Asn	Val	Thr
302	305					310					315		320
305	Ser	Glu	Thr	Asp	Ser	Arg	Pro	Asn	Arg	Ala	Asn	Ser	Leu
306				325				330				335	
309	Val	Leu	Leu	Val	Gln	Ser	Ser	Asn	Lys	Ser	Asn	Arg	Asn
310				340				345				350	
313	Ile	Ser	Asp	Pro	Asn	Leu	Asn	Ser	Ser	Ile	Ser	Leu	Lys
314				355				360				365	
317	Glu	Asp	Thr	Ala	His	Asn	Ser	Leu	Thr	Ser	Gln	Glu	Asn
318				370				375				380	
321	Gln	Val	Thr	Thr	Thr	Ser	Leu	Ser	Asn	Met	Thr	Val	Ala
322	385					390					395		400
325	Arg	Thr	Asp	Thr	Pro	Arg	Glu	Ile	Asn	Gly	Leu	Val	Asp
326				405				410				415	
329	Thr	Asn	Gly	Asn	Glu	Lys	Phe	Ser	Val	Glu	Ile	Met	Asn
330				420				425				430	
333	Lys	Ile	Gly	Leu	Asn	Pro	Lys	Ser	Phe	Thr	Asp	Glu	Glu
334				435				440				445	
337	Leu	Thr	Leu	Phe	Arg	Asn	Pro	Met	Arg	Leu	Ser	Ser	Glu
338				450				455				460	
341	Ser	Ser	Asn	Gly	Phe	Ser	Ile	Ala	His	Pro	Asn	Asn	Ser
342	465					470					475		480
345	Pro	Pro	Ser	Leu	Gln	Gly	Ile	Leu	Asn	Ala	Glu	Asp	Arg
346				485				490				495	
349	Ile	Glu	Pro	Ser	Arg	Ser	Ser	Phe	Ala	Thr	Asn	Asp	Thr
350				500				505				510	
353	Asn	Asn	Leu	Glu	Leu	Leu	Ser	Ser	Val	Thr	Asn	Leu	Lys
354				515				520				525	
357	Glu	Asn	Asp	Arg	Val	Thr	Lys	Thr	Gln	Ser	Arg	Arg	Glu
358				530				535				540	
361	Lys	Arg	Arg	Arg	Lys	Ala	Arg	Ile	Gln	Glu	Thr	Ser	Glu
362	545					550					555		560

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365 Val Val Asn Glu Pro Asn Glu Lys Pro Asp Gly Arg Ser Arg Arg Glu
366                               565                               570                               575
369 Arg Lys Lys Val Asn Tyr Ala Leu Pro Gly Leu Arg Thr Lys Leu Arg
370                               580                               585                               590
373 Arg Asn Phe Asp Leu Pro Ser Asp His Val Lys Ala Lys Lys Thr Arg
374                               595                               600                               605
377 Arg Ala Pro Lys Asn Ser Glu Asn Asp Ser Ala Thr Lys Thr Glu Thr
378                               610                               615                               620
381 Ala Asn Ile Thr Ser Glu Ala Pro Thr Thr Ser Glu Val Thr Leu Glu
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386                               645
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390 <211> LENGTH: 1773
391 <212> TYPE: DNA
392 <213> ORGANISM: yeast
394 <400> SEQUENCE: 5
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399 gaaaacatca gacagtcgta ttcgaggcaa aactccctgc tggccaagga taactccata      180
401 ttaaaaaatta agttaatag cttggaaaaa aaaataagcc agctggtaca agaaaacgtg      240
403 actctacgat ctaaaacctc tataagcgaa gctatctaca ggggaacggtt aagtaatcaa      300
405 ctacaagtca ttgaaaacgg tattattcaa agatttgacg aaatttttta tatgtttgag      360
407 aacgtacgta aaaacgaaaa tttgccagtg tcgagcttaa gaacaatggt gaagagaacg      420
409 agttccaggt caagatcatg ctcatgtgca tcaccacat actcaaaaag ttacactagg      480
411 ttatcaaata acgagaataa cctgtcgcgt gaatcaagtt ttaacaagga cgatggtcca      540
413 gatcttgagc ctaaggctaa aaaaaggaag agttctaggc ggcaatctat gtttgtatcc      600
415 acgagtttag aacctgaaga cgaaaccggt gaaaacgaac ccatgatgga aaattcctct      660
417 gtagaggtac cggcagaatc acacgagtc gcgcaagtgg aggaaacaat agatgcctta      720
419 aaccctgaag aggaaaatag cgattctgtc agtaatttta ccaattcaat tatagaatac      780
421 tccataccag aggagaatcc gacagaaccc gagcattcat cttctaaact agaaatatcc      840
423 aatgacagta caaatatgct aagtacagtg ccgtcaaata ctttgccggt gcctttacca      900
425 ggcccatccg caactttacc tactaccact agcgatgctt caacggtcta tccttcatca      960
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431 agcgaaatat catttacgag aactagaaga actcgtggta aagctgtaga ttacactttg      1140
433 ccttctttta gagccaaaat gaggaggcct tcagaaaaac ttgtggatgc tactactgtg      1200
435 attgatatac atgatctaca ggtttccaag agaaatcggg aaacttcaca taaaaggaaa      1260
437 agtttatccc aagattcaat acccgacgaa ccgcaattga gagaagtcgt cgtctcaaag      1320
439 gattatggaa ctccaaaagg gaaaaaaacg gaagatgaaa tacacgagga taccgctcat      1380
441 ctaatgacca cttccaacaa caacagcaac aacaaaaacg aaaaaaaact aactagcaac      1440
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445 aagtcaacaa gaactaaaaa attgttcaaa aatgcaattg tcaataattt atctgatgaa      1560
447 aattctacta cgcgaccctc caagtcgtca aagggaacca gtaataataa caacaattac      1620
449 aacaatttcg acaataacaa ttcaaacatt aataatgtta ataataaatc tgttagcttt      1680
451 agactaaatg aagatgattt agcagtattt gatttatttg gaaatggtaa ggcagtgaaa      1740
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456 <210> SEQ ID NO: 6
457 <211> LENGTH: 590

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:40

**VERIFICATION SUMMARY**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date